

Met	9P	9N	6P	6N	ABT	Expression ratio to mean ABT
Gene	UniGene	Met	9P	9N	6P	6N
TGM4	Hs.2387	32.70±21.83	17.46±21.27	12.50±17.11	5.23±3.92	23.47±19.76
ZFP38	Hs.343588	4.68±3.55	1.98±1.34	2.03±1.94	1.58±1.53	4.05±1.83
RIS1	Hs.35861	4.07±4.35	2.79±3.19	2.03±3.95	2.19±6.53	2.05±2.03
EFS2	Hs.24587	7.37±1.91	1.68±0.75	2.03±0.38	1.82±0.44	2.81±0.70
FLH2	Hs.6302	3.18±1.28	1.79±1.20	1.82±1.72	2.88±2.71	2.38±2.31
FOXP1	Hs.107948	3.73±2.16	2.21±1.10	1.42±0.92	3.19±2.26	2.88±2.18
ENIGMA	Hs.155591	8.43±4.01	2.34±1.42	2.19±0.87	3.19±2.43	3.28±3.05
FHL1	Hs.219069	5.25±2.69	1.94±0.87	1.82±0.97	3.40±1.71	2.78±1.65
PCP4	Hs.30798	32.49±17.40	3.06±1.64	2.38±1.51	5.22±4.09	3.38±14.14
ON1	Hs.4222	3.23±2.61	4.59±1.95	3.12±1.38	5.17±3.60	4.09±2.72
TMALN	Hs.301961	9.40±4.84	3.45±1.68	1.48±0.84	5.20±1.36	2.35±1.87
CSTP1	Hs.106180	7.89±2.31	3.02±1.60	2.07±0.69	5.92±0.91	3.39±2.66
ZNF185	Hs.1622	11.17±4.38	3.23±1.50	2.83±0.80	5.15±1.28	3.48±1.80
TRIM20	Hs.62237	6.26±2.82	2.51±1.98	2.95±2.56	5.43±2.51	2.60±2.56
KRT5	Hs.195850	63.86±80.24	8.67±3.12	5.24±2.81	4.78±2.44	2.98±4.10
BPAG1	Hs.198689	14.04±6.03	3.75±1.74	5.03±4.19	4.14±2.10	2.76±3.82
PLP1	Hs.1787	5.09±3.00	2.54±1.74	2.08±2.45	3.01±2.75	2.21±2.43
PSP94	Hs.163752	129.56±59.19	3.18±2.12	4.14±1.34	2.38±1.84	2.88±1.84
LOC13148	Hs.57548	9.20±7.49	3.27±1.41	1.14±0.73	4.34±1.48	3.29±1.63
WFDC2	Hs.2719	11.21±3.80	2.71±1.62	4.35±2.78	5.24±2.49	3.14±2.64
NEFM	Hs.198760	14.89±7.11	17.22±14.17	4.59±1.85	2.95±1.74	1.69±0.75
MTG5	Hs.63342	50.71±213.95	6.38±3.01	5.24±5.63	4.68±5.26	4.45±4.94
CACNA1C	Hs.16520	63.85±47.88	2.98±0.84	3.39±0.69	1.59±0.48	3.58±0.85
ACSF5	Hs.1652	7.22±2.74	2.27±1.24	3.87±1.07	1.00±0.90	2.24±2.06
THNSB	Hs.56245	7.17±1.93	2.27±1.26	1.53±3.93	2.94±3.33	3.61±2.79
AMACR	Hs.126749	3.70±1.24	3.69±1.29	3.19±1.29	2.94±1.29	3.61±2.79
HPN	Hs.823	5.99±3.64	3.19±1.31	2.80±2.08	1.88±2.46	1.90±2.55
DKFZP564B167	Hs.76285	2.50±3.43	2.22±1.19	1.62±1.03	3.04±2.75	2.46±2.72
STEAP	Hs.61635	2.35±6.70	2.65±3.94	2.37±2.59	3.64±1.49	1.88±0.78
FOLH1	Hs.1915	3.76±10.12	2.61±3.17	1.80±2.11	3.14±1.89	3.01±2.15
CADPS	Hs.15130	10.26±11.52	2.30±2.56	1.04±0.52	0.25±0.19	1.13±0.40
LOC90355	Hs.25923	3.87±2.24	2.87±2.07	0.77±1.18	1.91±2.13	2.21±1.99
ERG2	Hs.43514	20.06±27.86	8.36±9.15	4.88±5.49	5.06±7.52	19.69±12.87
MACMARCKS	Hs.75061	3.08±12.35	2.62±4.51	2.45±7.68	2.95±4.70	4.02±2.80
GTBP	Hs.116651	4.79±1.19	3.73±0.89	1.78±1.88	2.01±2.39	1.34±1.20
NAUD101	Hs.193367	5.21±5.52	3.45±5.83	2.05±0.91	2.76±0.95	2.90±0.49
TK1	Hs.75078	8.44±10.86	2.18±1.06	4.45±1.80	2.18±1.89	1.85±0.66
MAD2L1	Hs.55956	4.60±3.94	4.13±6.92	3.49±6.28	4.65±3.74	4.34±7.76
KIAA0306	Hs.55956	4.60±3.94	4.13±6.92	3.49±6.28	4.65±3.74	4.34±7.76
CCNB2	Hs.134698	5.04±7.95	4.05±11.25	2.10±2.29	3.47±3.83	3.93±2.65
BUB1B	Hs.103834	2.37±5.29	2.89±5.24	2.13±1.64	1.60±2.18	2.08±2.65
CCNB1	Hs.23980	4.31±2.88	3.07±6.25	2.12±2.07	2.24±0.82	2.13±1.05
DEEPEST	Hs.16244	5.12±1.55	3.71±7.67	2.23±1.37	1.62±1.52	2.11±1.49
KIAA0168	Hs.36232	5.32±3.32	2.91±2.60	1.43±0.52	2.42±1.13	1.16±0.98
TNRC9	Hs.110826	6.76±6.11	8.22±6.60	2.16±1.14	6.09±2.54	8.03±2.95
RAP2A	Hs.355373	3.87±9.42	1.24±1.51	0.81±0.68	0.83±1.21	1.44±0.67
FAR	Hs.120087	5.65±11.11	10.49±13.61	8.82±13.08	17.51±15.26	21.01±15.34
KAP-1alpha	Hs.356220	27.64±88.62	5.57±25.47	1.55±2.45	0.98±0.46	0.93±0.65
ARHGDI	Hs.83656	4.04±1.27	3.02±3.17	1.59±0.79	2.09±0.69	2.19±0.53

Fig. 1

2/23

Gene	Primers and Probe			Amplicon bp
ZNF185	FP	TGG ATG AAA GGC AAG GTA AAG AG		84
	RP	TTC TAA AAC TCC CTT AAA GGC AGA CT		
	Probe	CCA AGA TAG GCT GGC TTC CCC CG		
PSP94	FP	AGT GAA TGG ATA ATC TAG TGT GCT TCT AGT	100	
	RP	GCA TGG CTA CAC AAT CAT TGA CTA T		
	Probe	CCC AGG CCA GGC CTC ATT CTC CT		
BPAG1	FP	TCG CTG AAA GAG CAC GTC AT		94
	RP	AGC AAT CTA AAA CAC TGC AGC TTG		
	Probe	AAT CAA AGA GAA AGA TAT AAA TTC GTT CCC ACA GCC		
Erg-2	FP	TCC TGT CGG ACA GCT CCA AC		75
	RP	CGG GAT CCG TCA TCT TGA		
	Probe	TGC ATC ACC TGG GAA GGC ACC AAC		

Fig. 2a

3/23

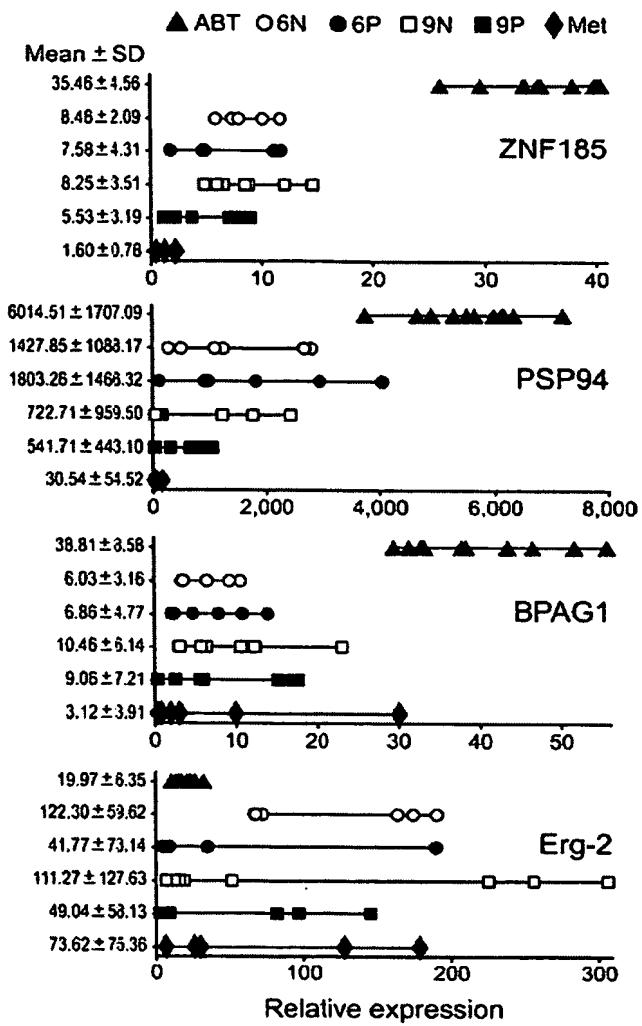


Fig. 2b

4/23

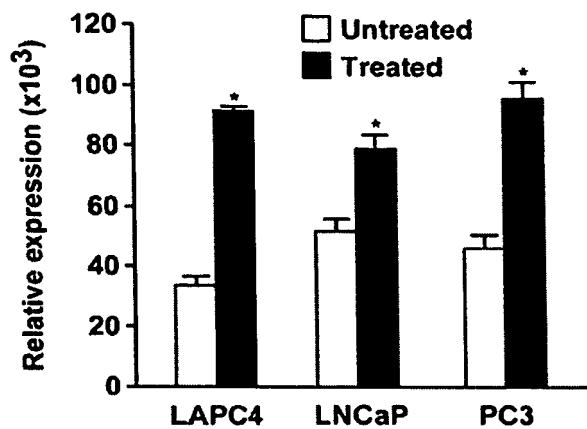


Fig. 3a

Primer set			Size (bp)	Genomic position
1 W	FP	GCGCAGTTCCGGGTGTCTGTC	197	210
	RP	GC GGGG AGGACCAGCGTTAG		
1 M	FP	GCGTAGTT CGGGTGTGTTG	197	210
	RP	AC <u>GG</u> AAAAAAACCAAC <u>GG</u> TTAACTA		
1 U	FP	GTGTAGTT IGGGTGTGTTGTTAGG	198	210
	RP	C AAAAAAACCAAC <u>AT</u> TAACTATTCTC		
2 W	FP	CCTGGGACTCCGTCA <u>G</u> ACTGG	146	336
	RP	GACAGACACCC <u>GG</u> ACTGCG		
2 M	FP	TT GGGATTT <u>CG</u> TTAGATTGG	145	335
	RP	AACAAACACCC <u>GA</u> ACTACG		
2 U	FP	TGGGATTT <u>GT</u> TAGATTGGAAAGG	146	333
	RP	CTAACAAACACCC <u>AA</u> ACTAC <u>CC</u> A		

Fig. 3b

6/23

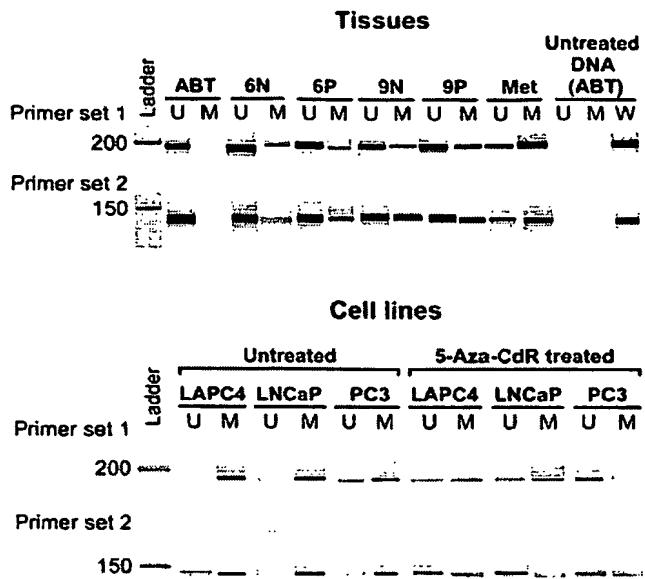


Fig. 3c

7/23

Samples	Total	Methylated (%)
Benign prostatic tissues	12	0 (0)
Gleason Score 6 tumors	11	4 (36.3)
Gleason Score 9 tumors	14	7 (50)
Metastatic tissues	5	5 (100)

Fig. 3d

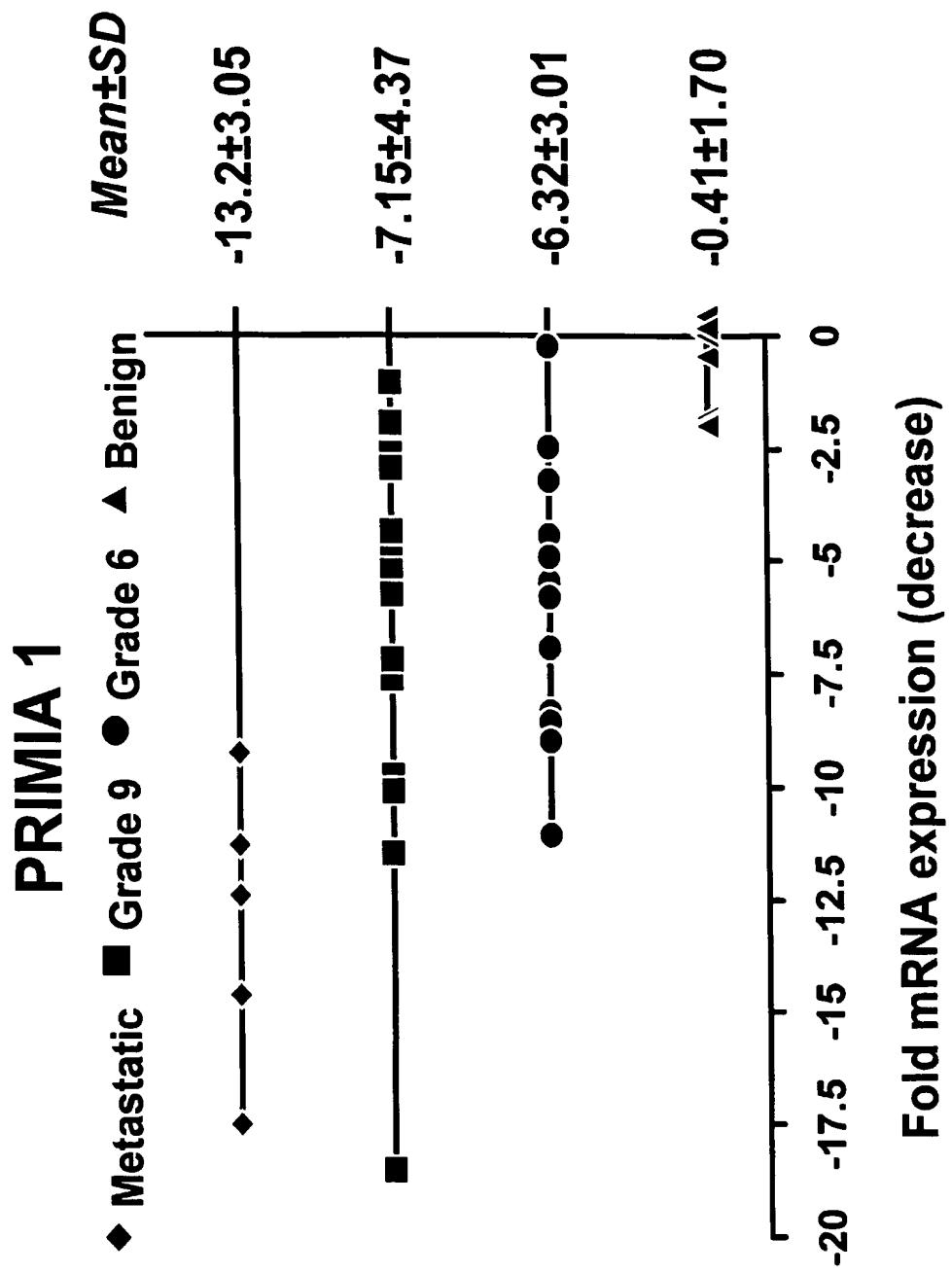


Fig. 4

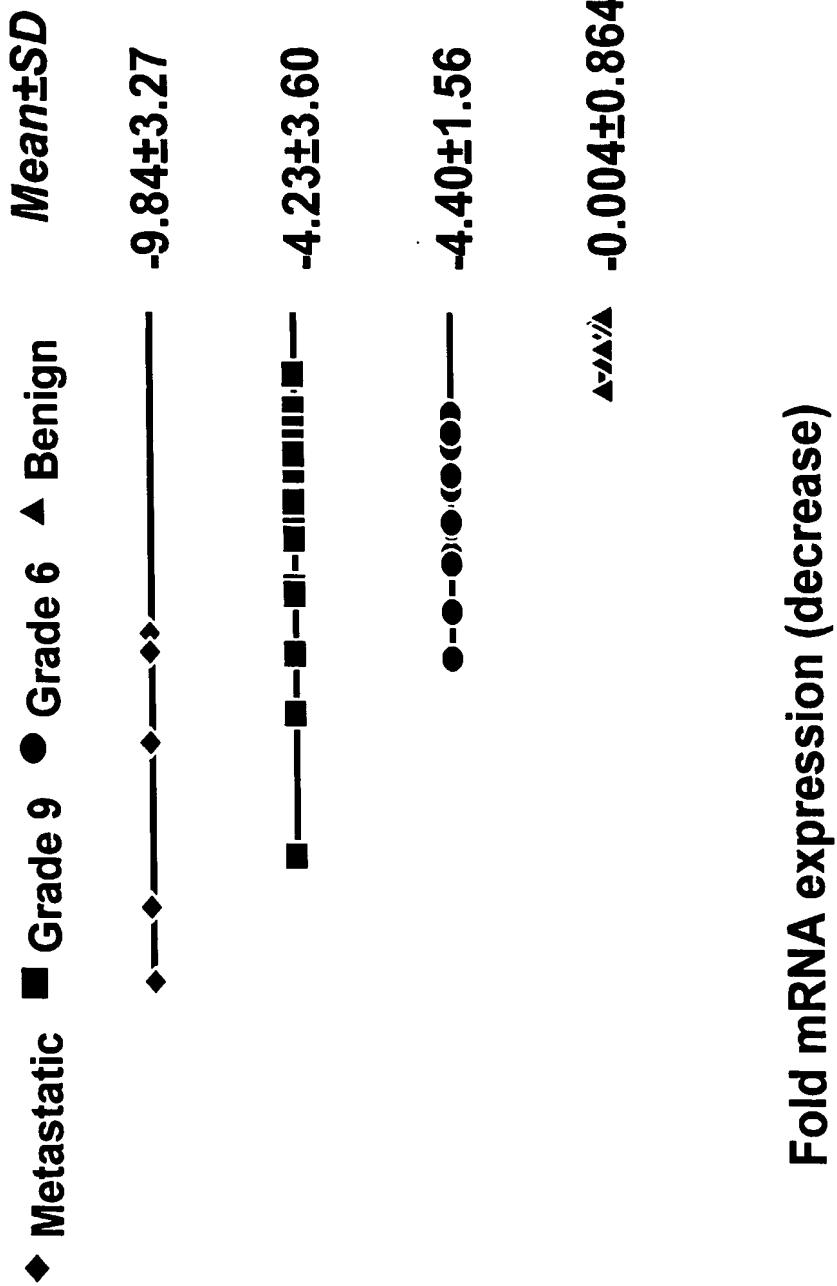


Fig. 5

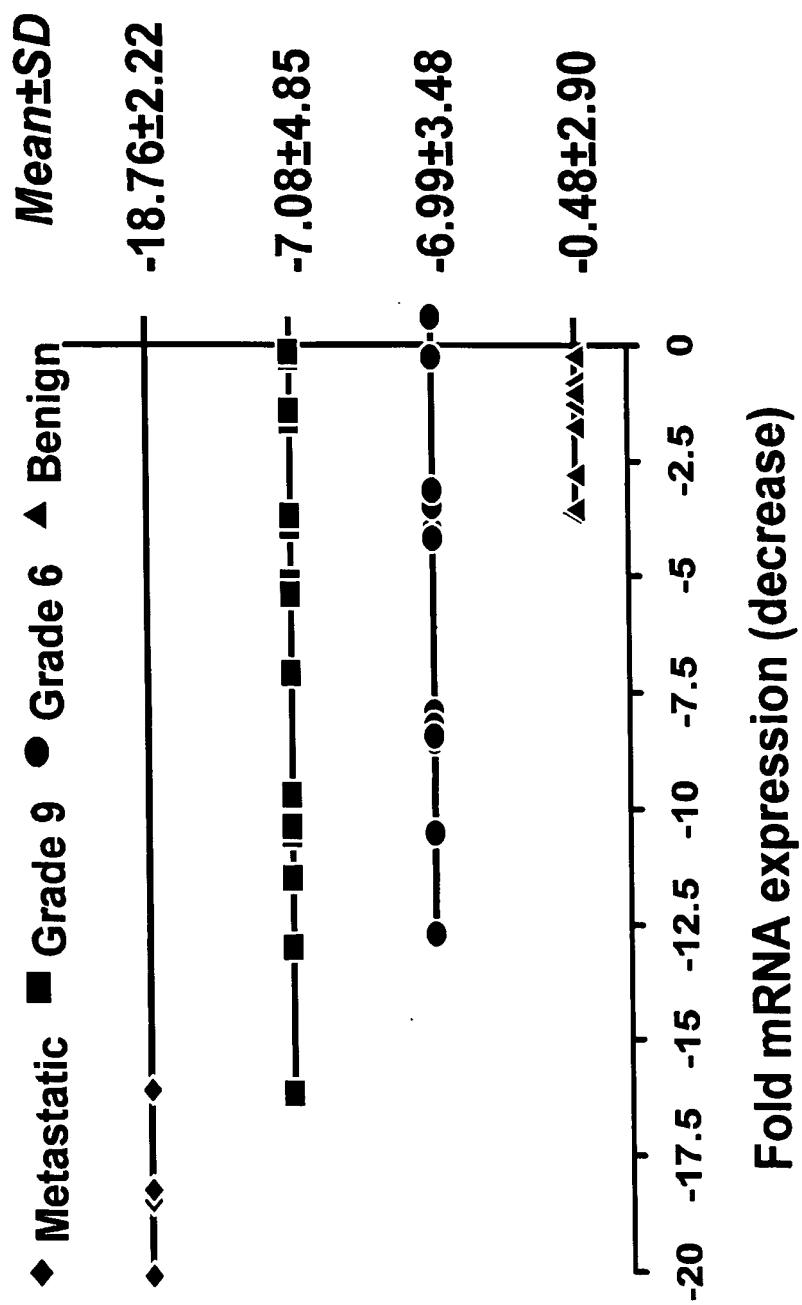


Fig. 6

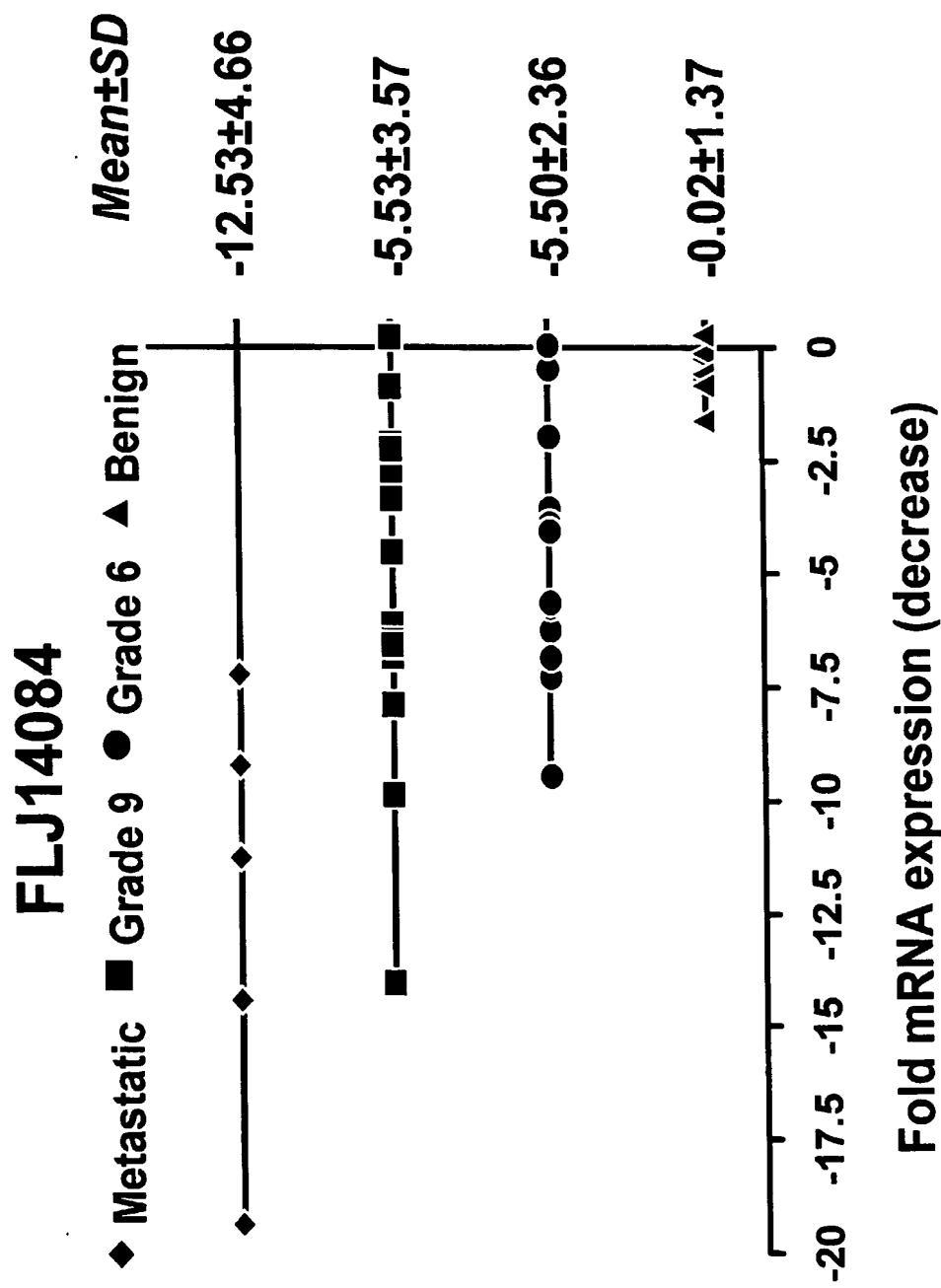


Fig. 7

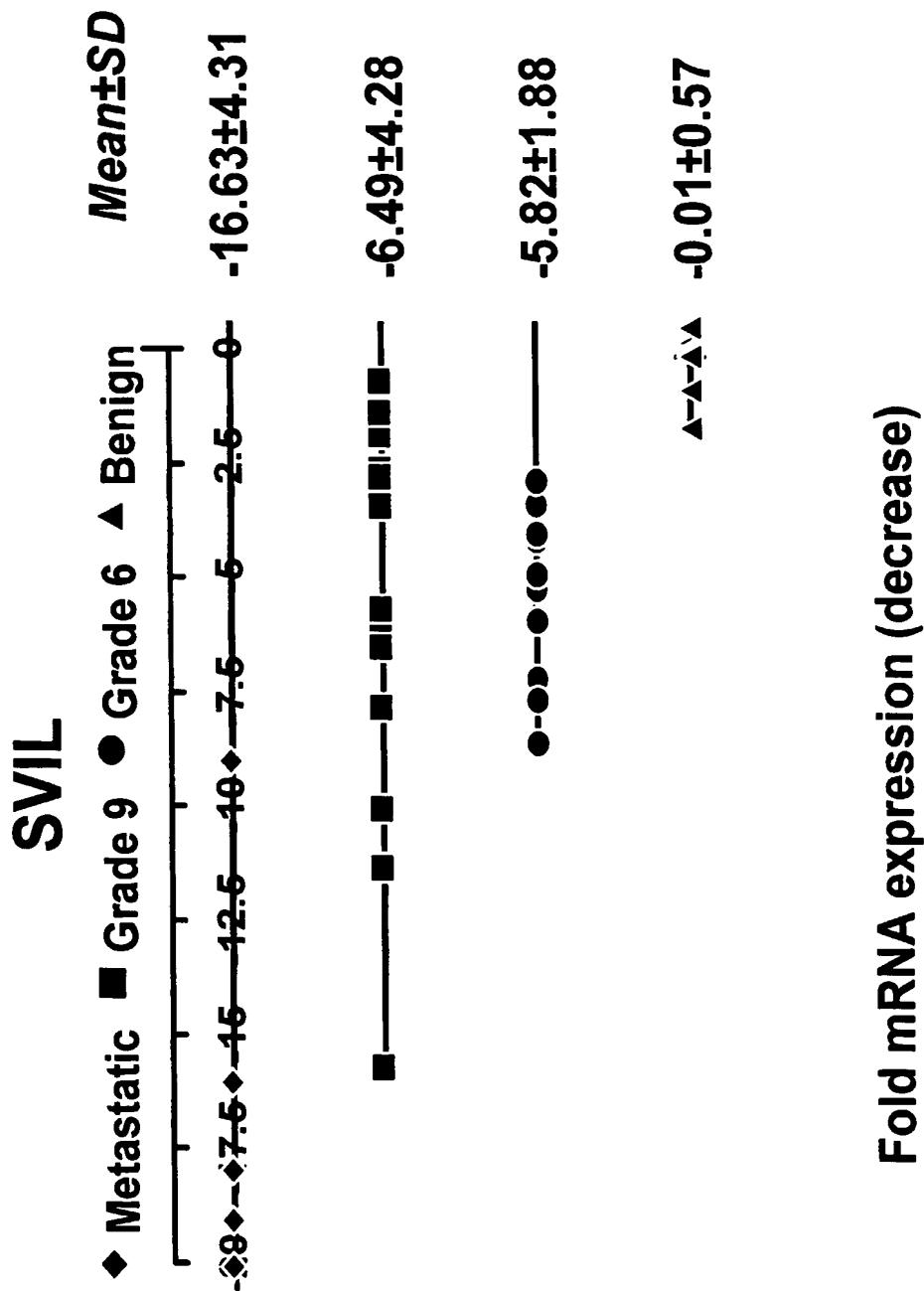


Fig. 8

13/23

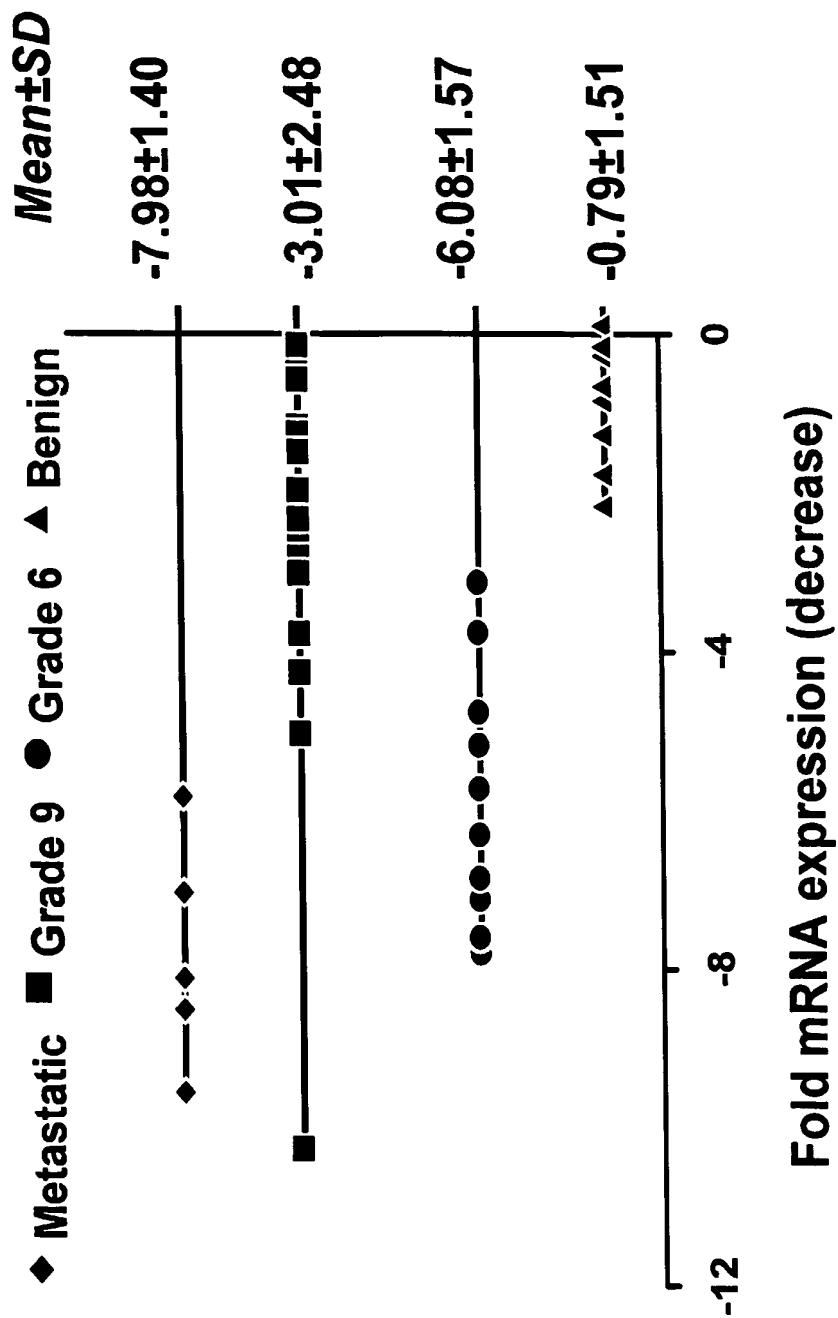


Fig. 9

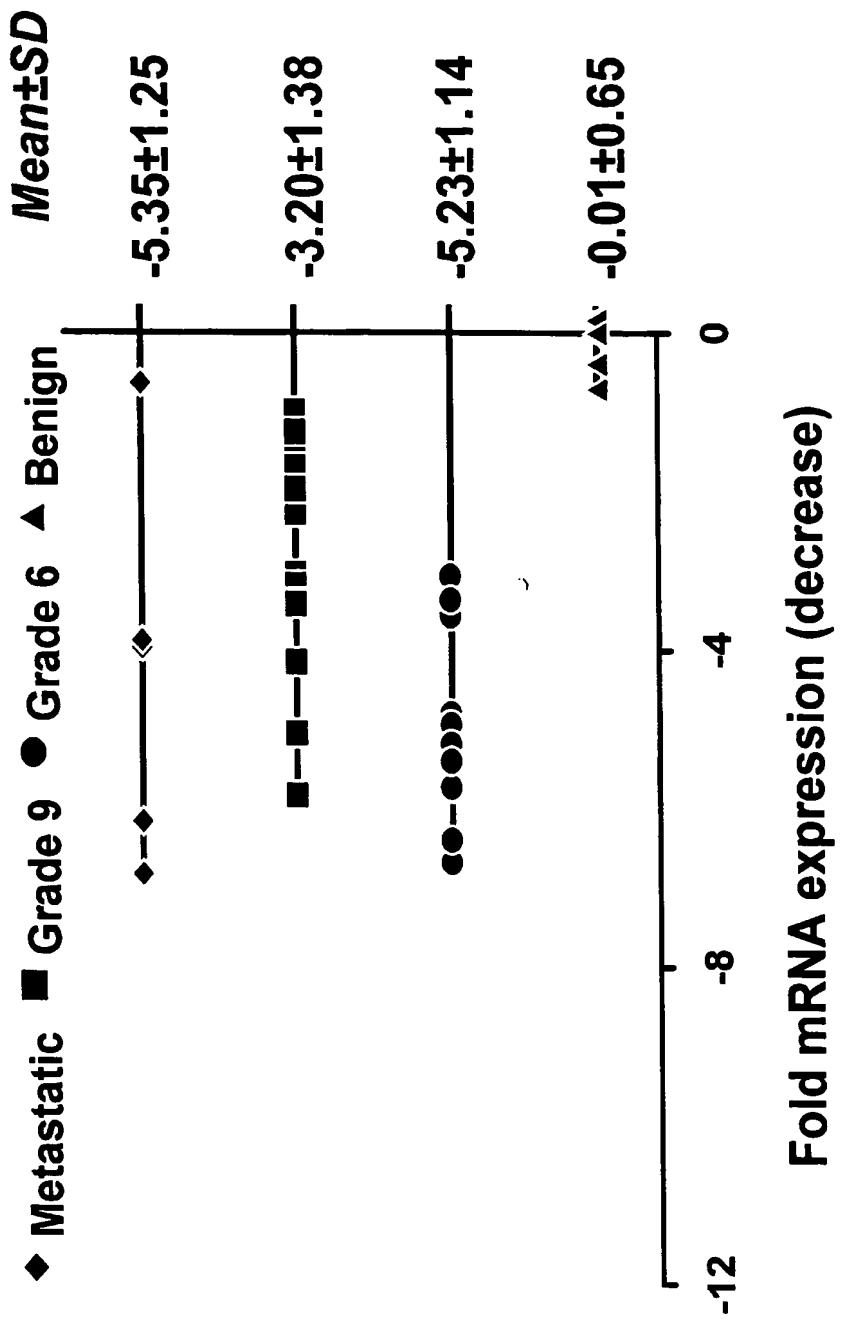


Fig. 10

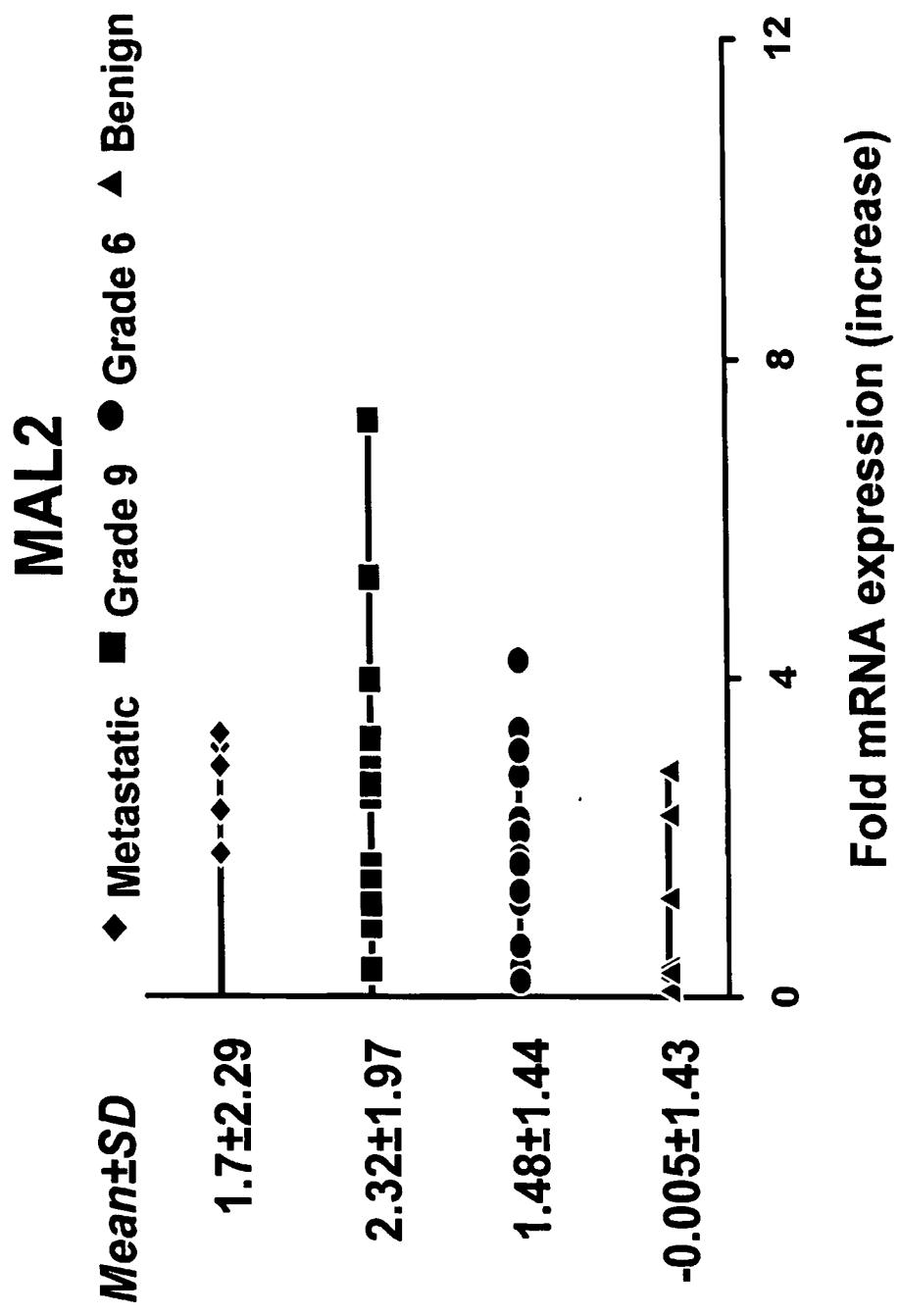


Fig. 11

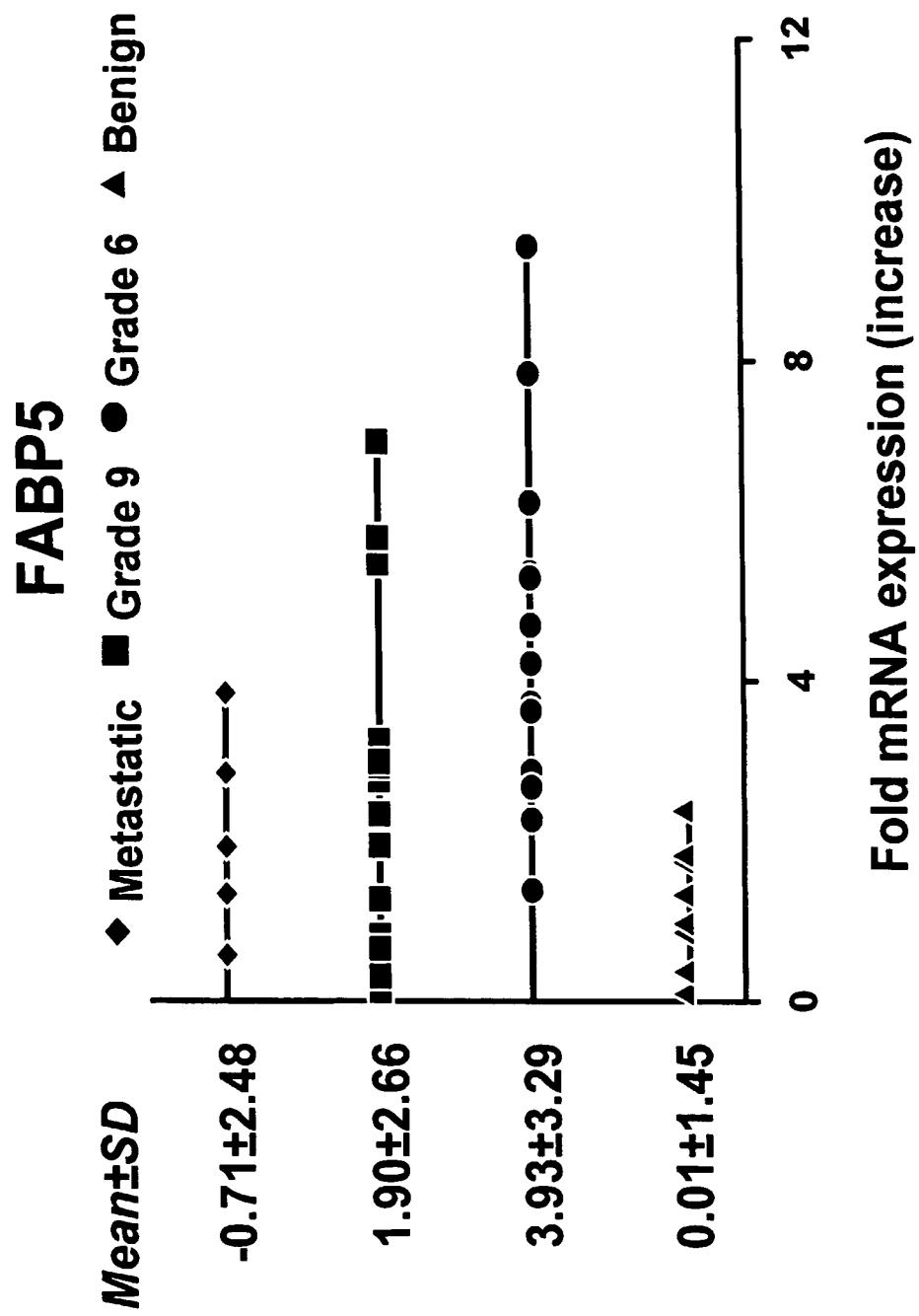


Fig. 12

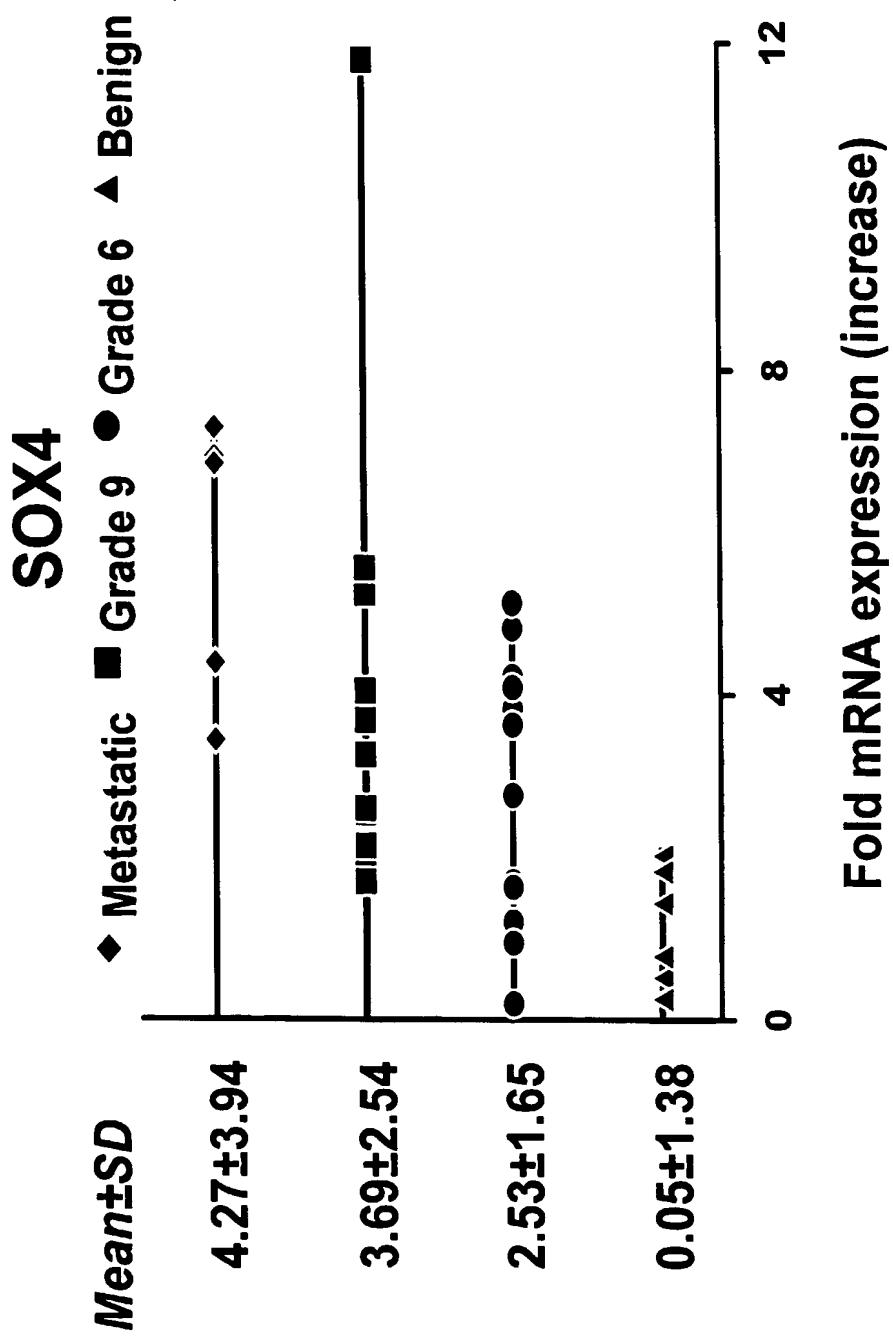


Fig. 13

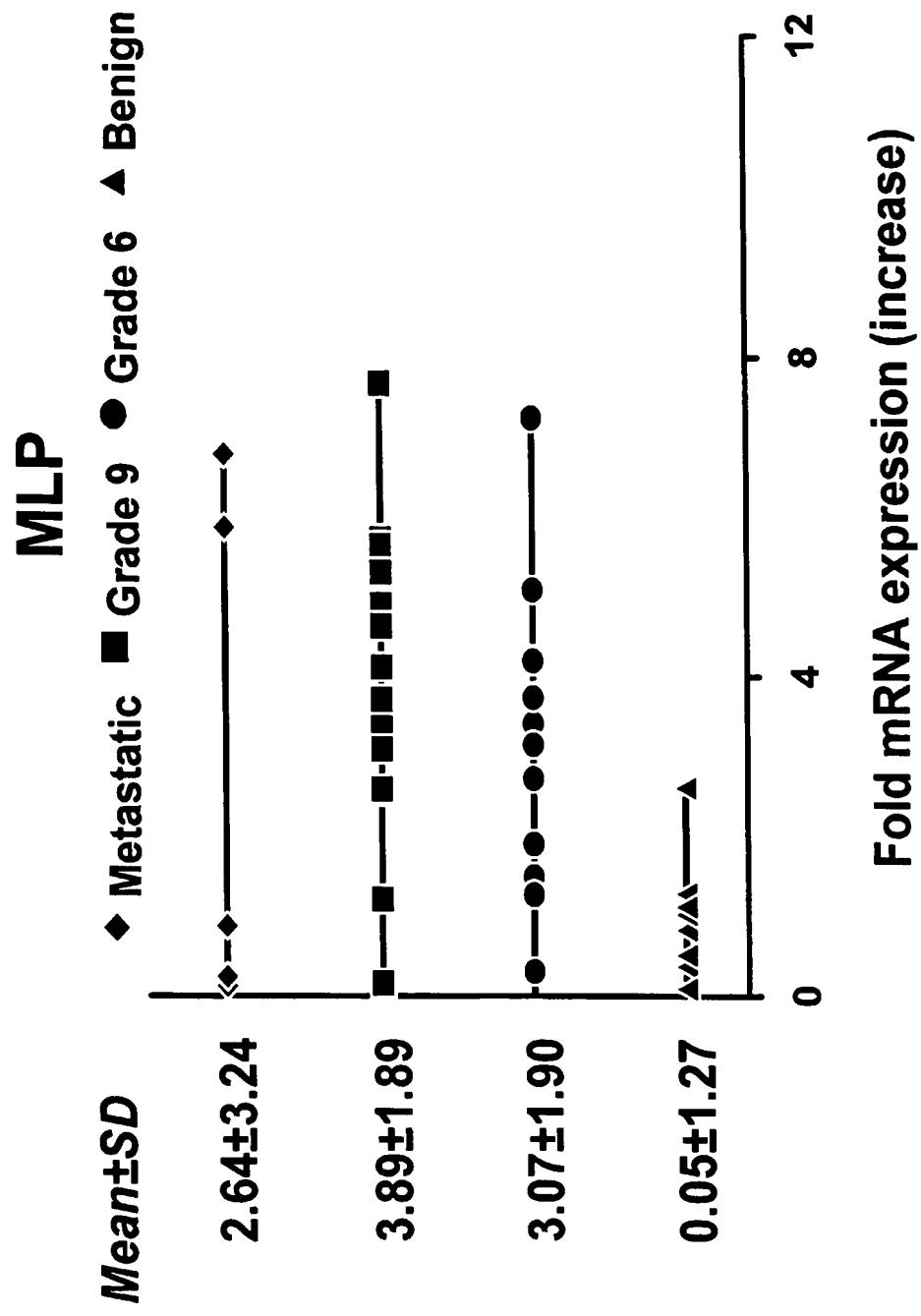


Fig. 14

19/23

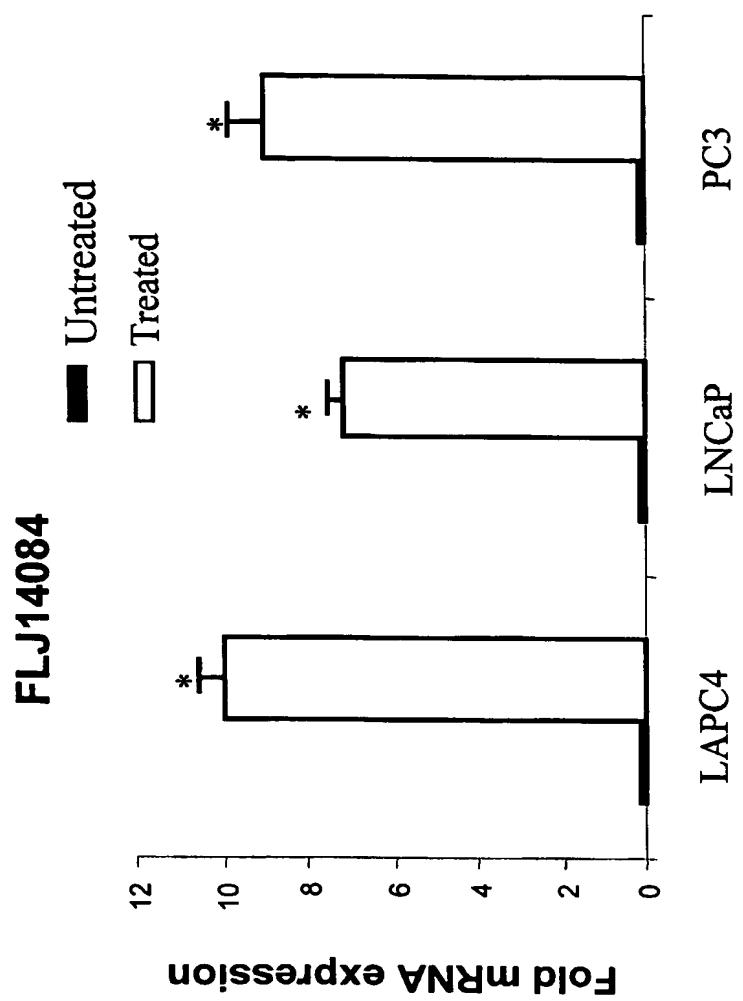


Fig. 15

20/23

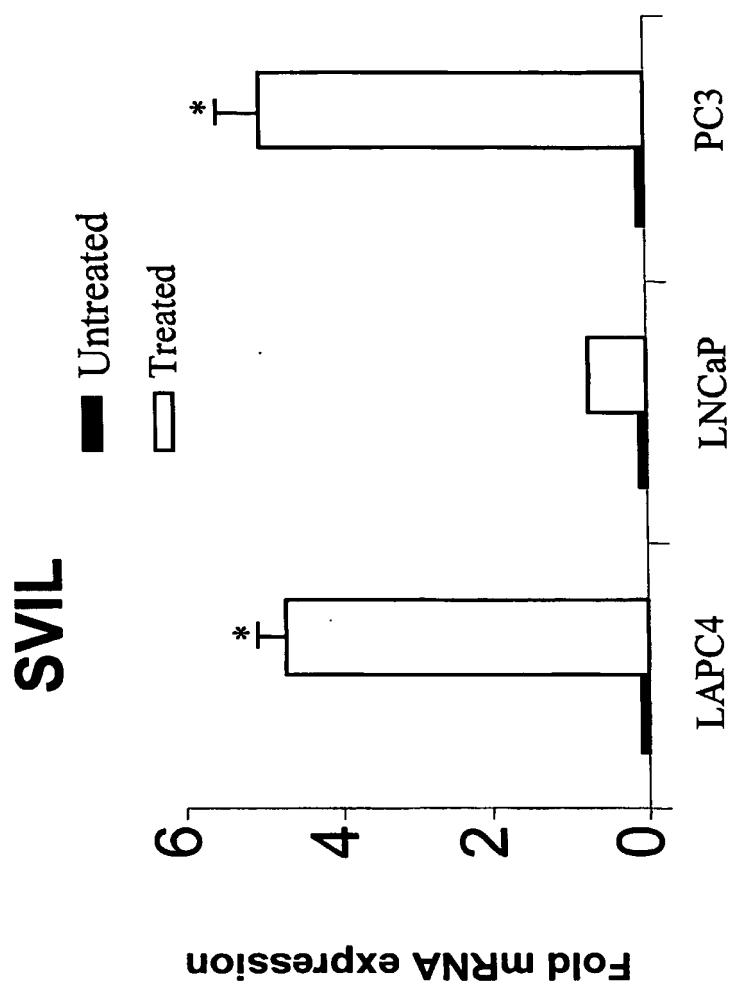


Fig. 16

21/23

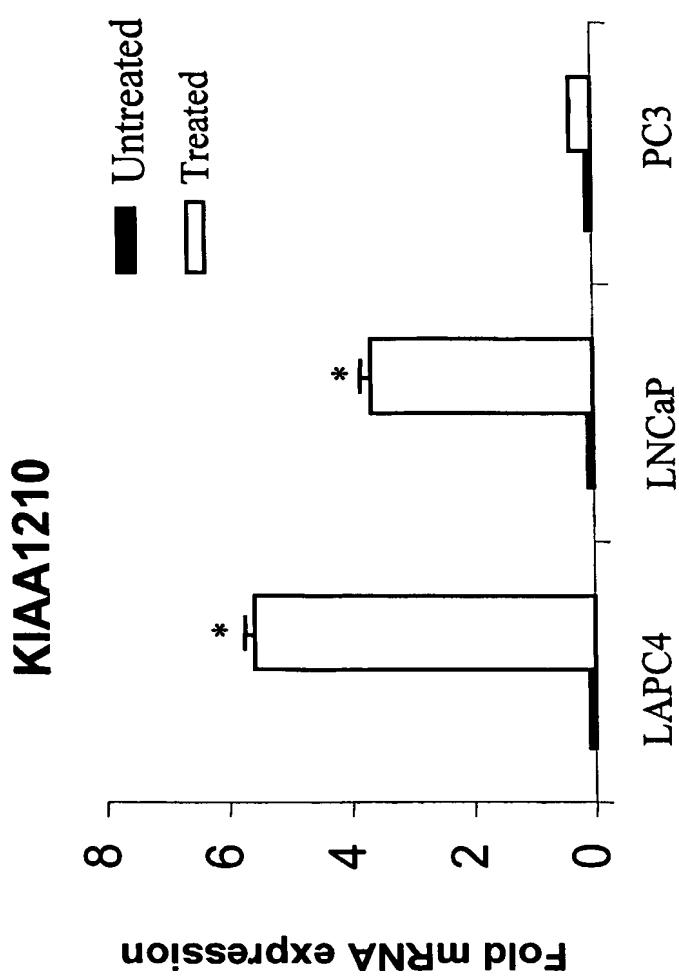


Fig. 17

22/23

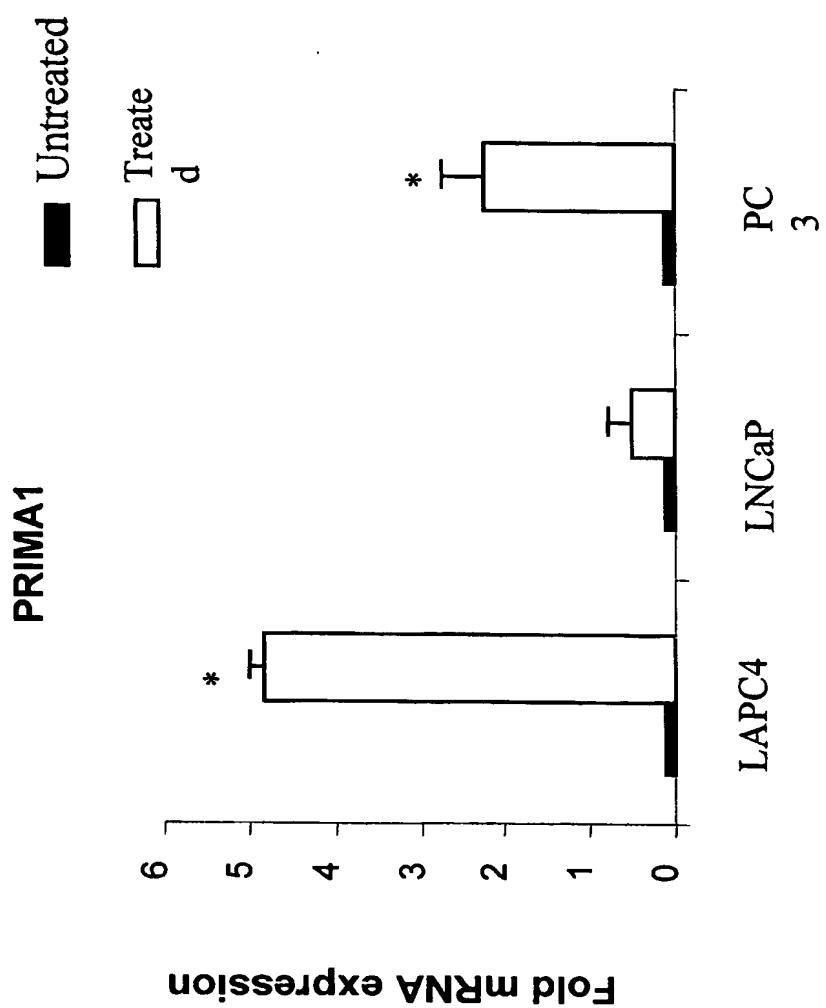


Fig. 18

23/23

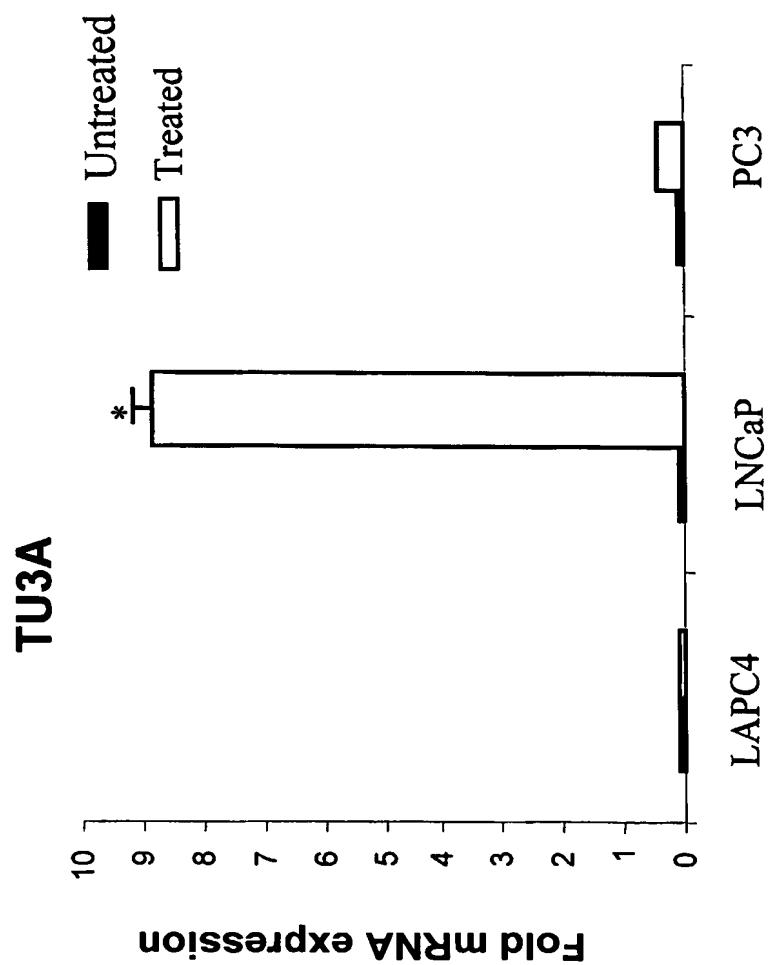


Fig. 19